

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2017/08/14 17:40:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/home/bethany/projects/planctomycetes+halococci/QC/Gem_CJuql4.sorted.b
am -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	blasr ../pachio_raw/G05_1/Analysis_Results/m150527_194555_42153_c100830882550000001823183611251586_s1_p0.bas.h5 ../assembly/final_contigs/Gem_Juql4_final_contigs.fasta --sam --out Gem_CJuql4.sam --nproc 16
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	1 (5.3.574e1c2)
Analysis date:	Mon Aug 14 17:38:45 NZST 2017
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	/home/bethany/projects/planctomycetes+halococci/QC/Gem_CJuql4.sorted.bam

2. Summary

2.1. Globals

Reference size	7,944,162
Number of reads	250,189
Mapped reads	250,189 / 100%
Unmapped reads	0 / 0%
Mapped paired reads	0 / 0%
Read min/max/mean length	44 / 38,823 / 7,320.04
Duplicated reads (estimated)	42,866 / 17.13%
Duplication rate	8.31%
Clipped reads	250,185 / 100%

2.2. ACGT Content

Number/percentage of A's	130,891,357 / 15.76%
Number/percentage of C's	276,762,473 / 33.32%
Number/percentage of T's	130,453,619 / 15.71%
Number/percentage of G's	276,147,128 / 33.24%
Number/percentage of N's	0 / 0%
GC Percentage	66.56%

2.3. Coverage

Mean	109.2161
Standard Deviation	55.4677

2.4. Mapping Quality

Mean Mapping Quality	229.69
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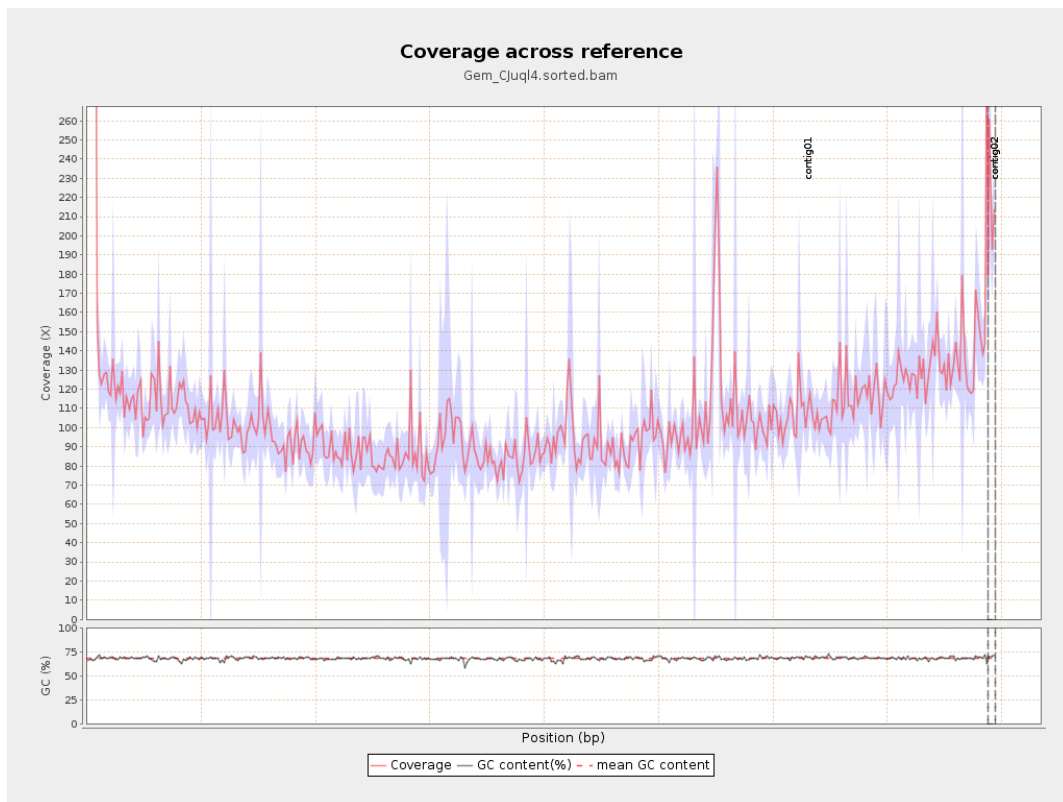
2.5. Mismatches and indels

General error rate	18.13%
Insertions	73,418,334
Mapped reads with at least one insertion	99.58%
Deletions	33,898,264
Mapped reads with at least one deletion	98.54%
Homopolymer indels	18.14%

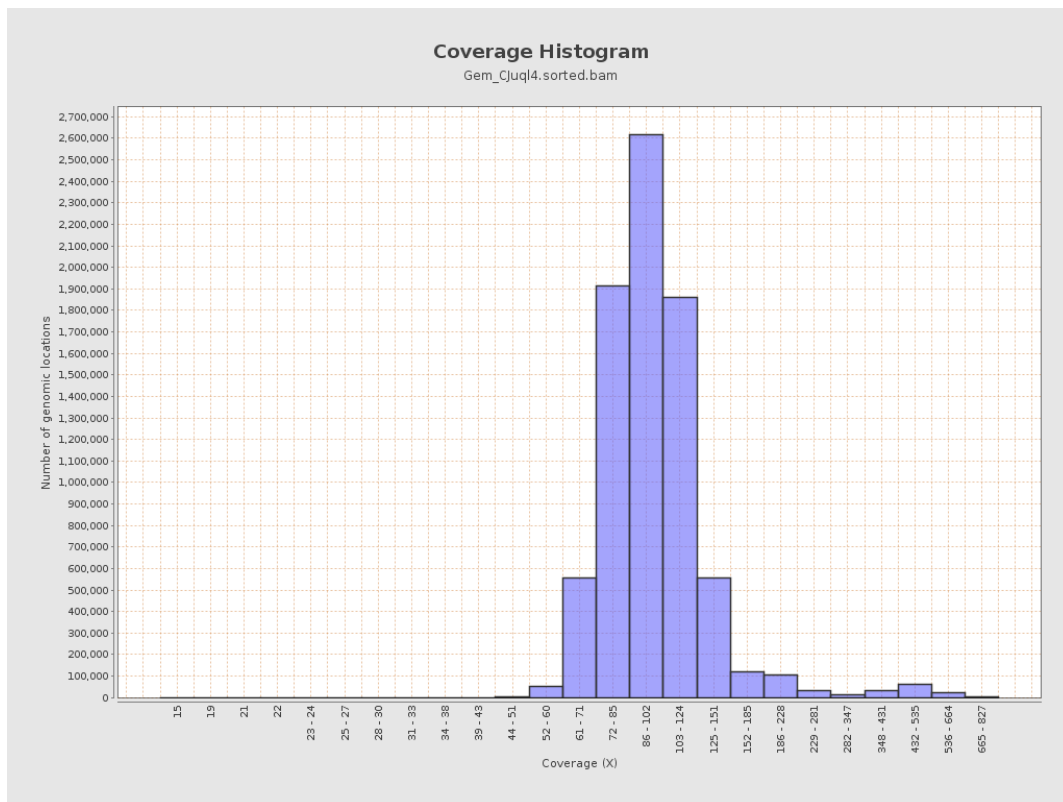
2.6. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation
contig01	7884659	854406556	108.3632	54.722
contig02	59503	13224111	222.2428	47.9505

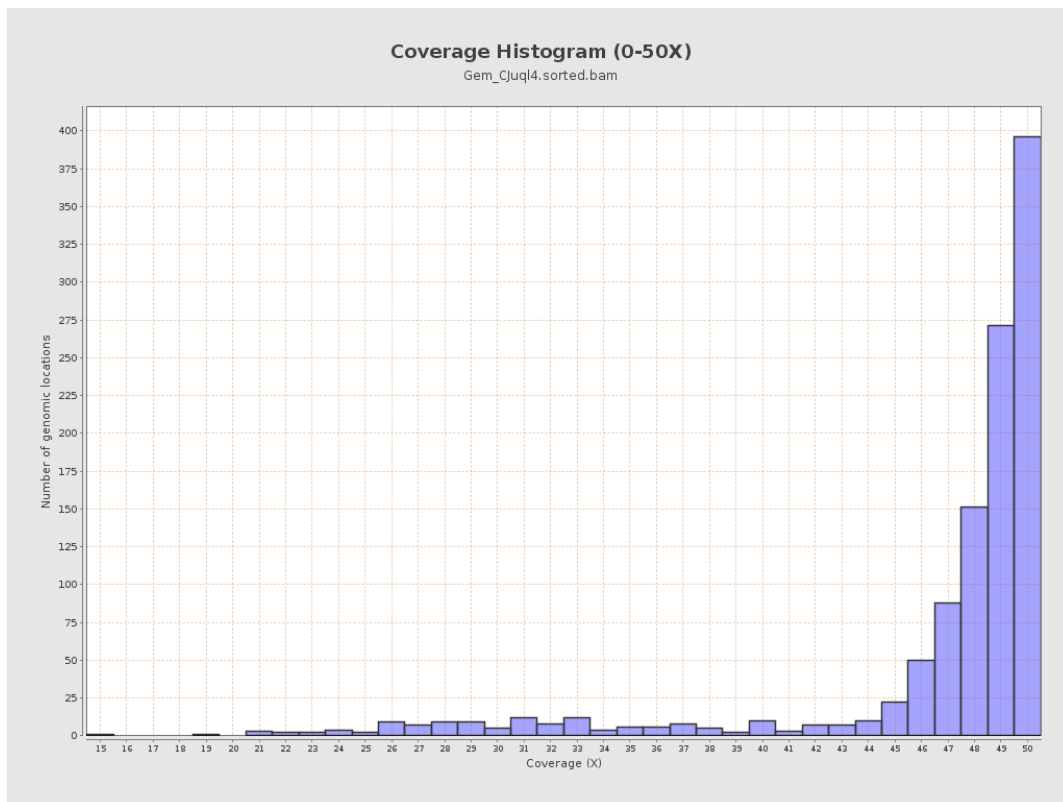
3. Results : Coverage across reference



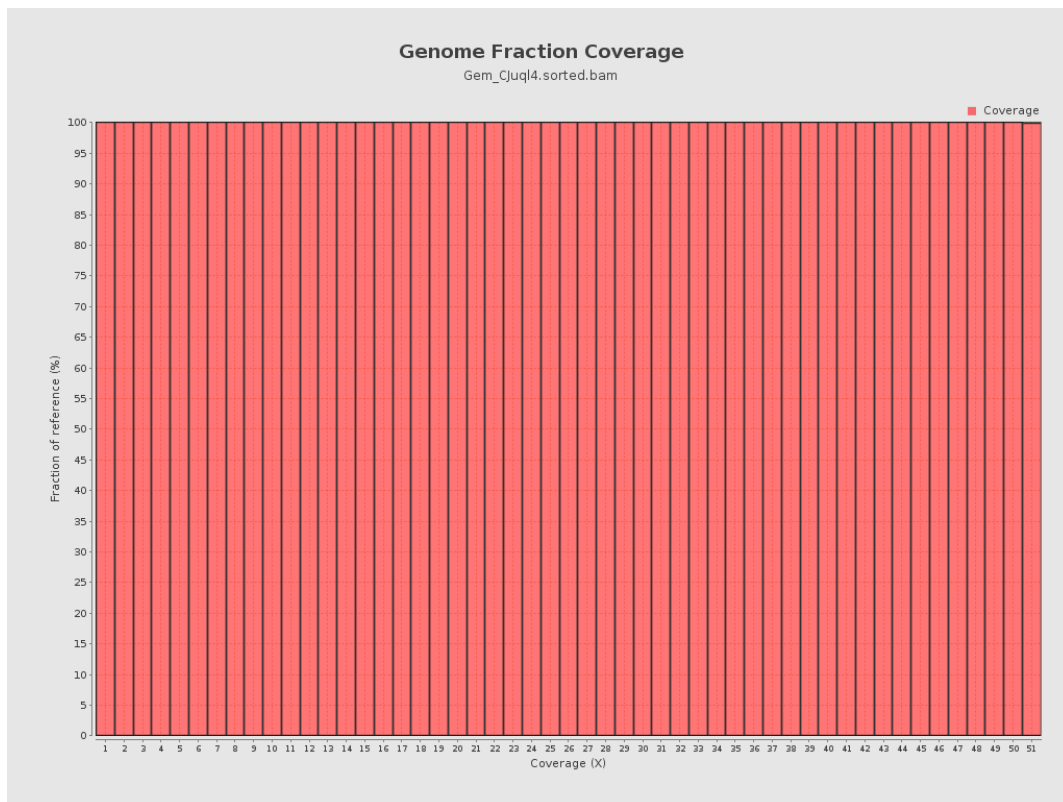
4. Results : Coverage Histogram



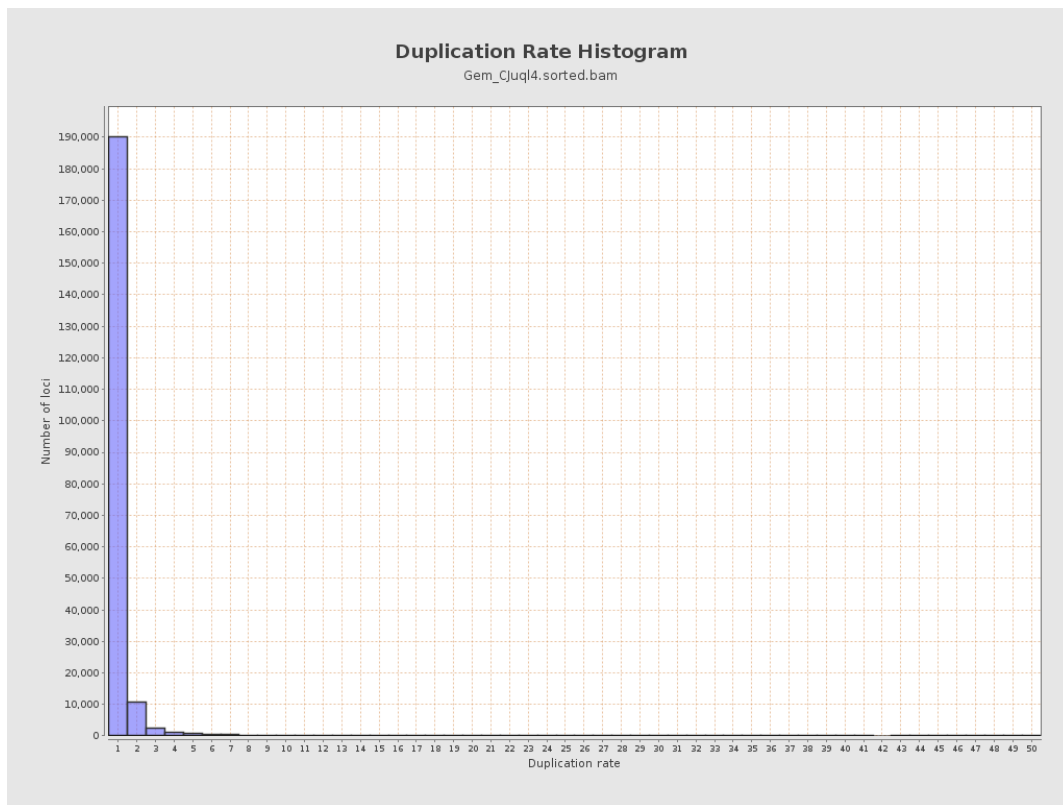
5. Results : Coverage Histogram (0-50X)



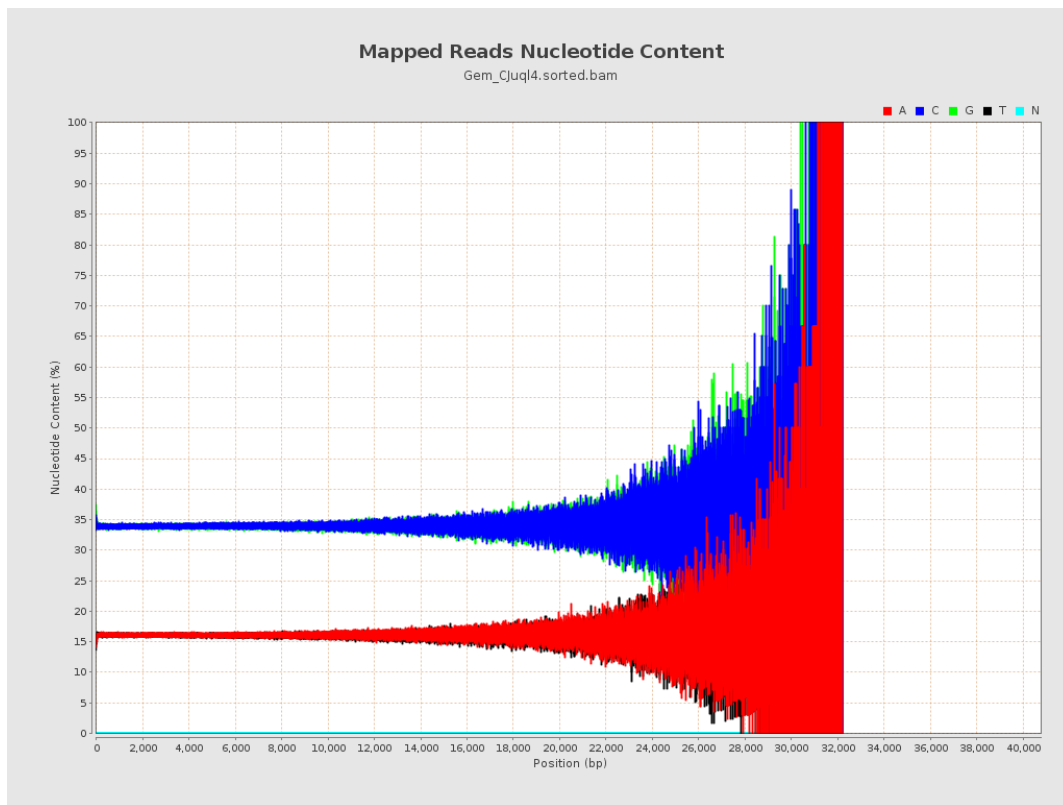
6. Results : Genome Fraction Coverage



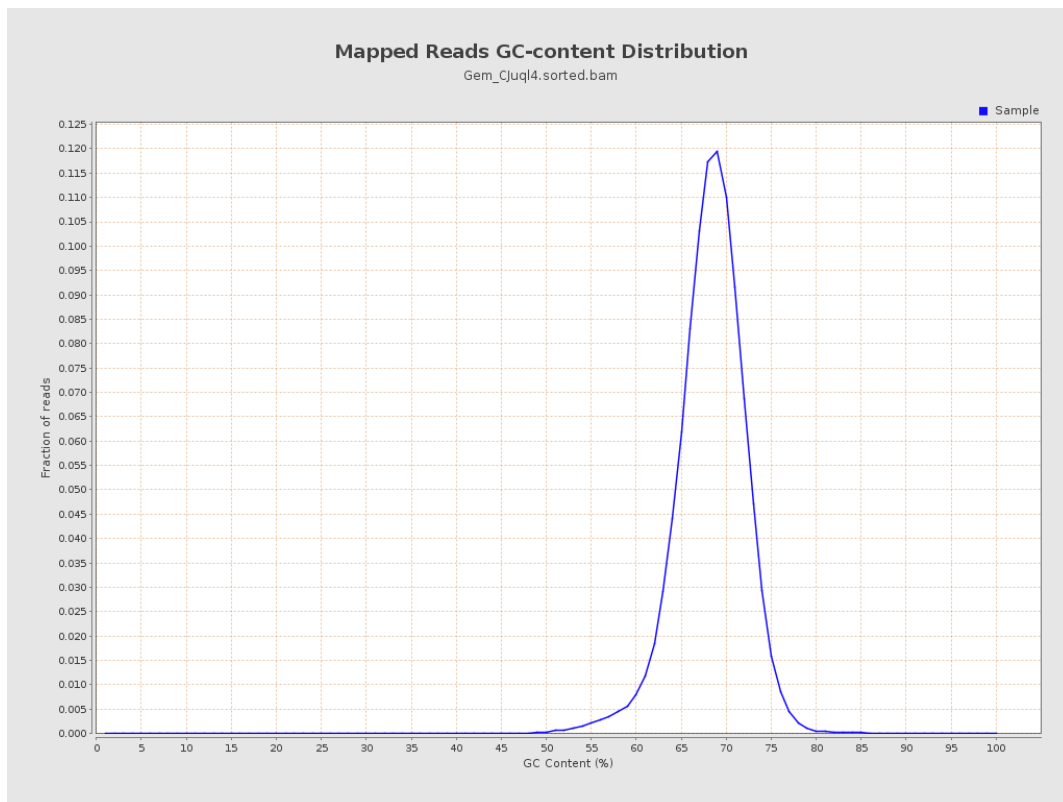
7. Results : Duplication Rate Histogram



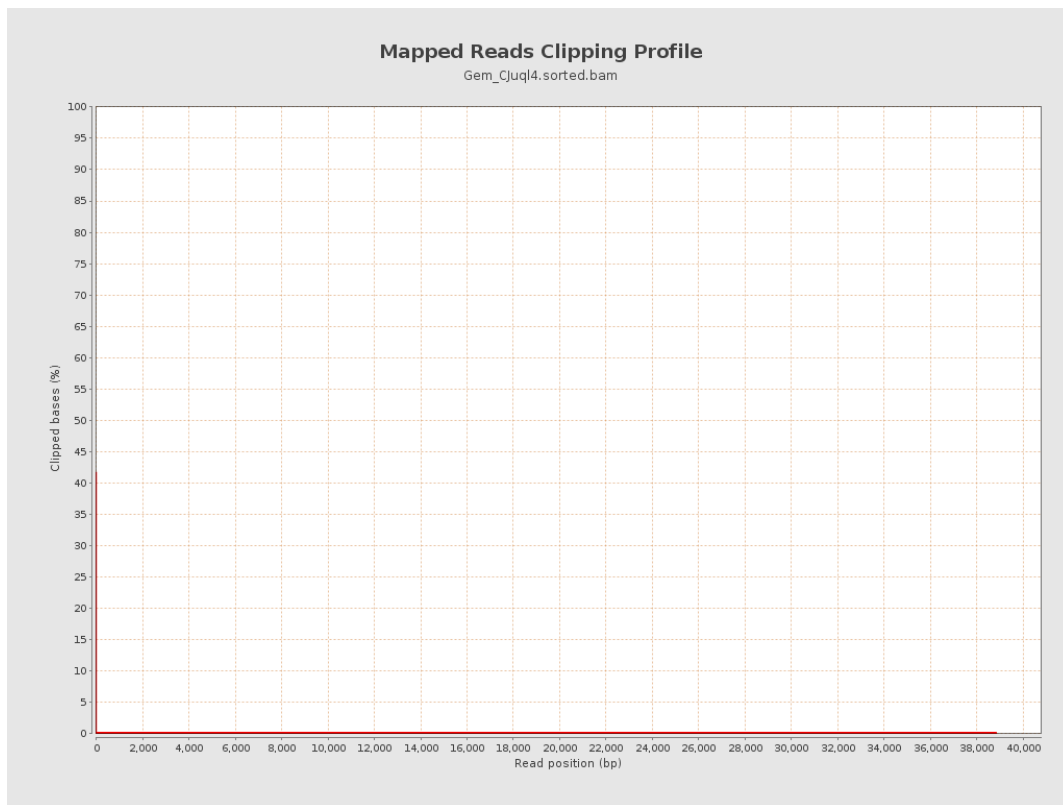
8. Results : Mapped Reads Nucleotide Content



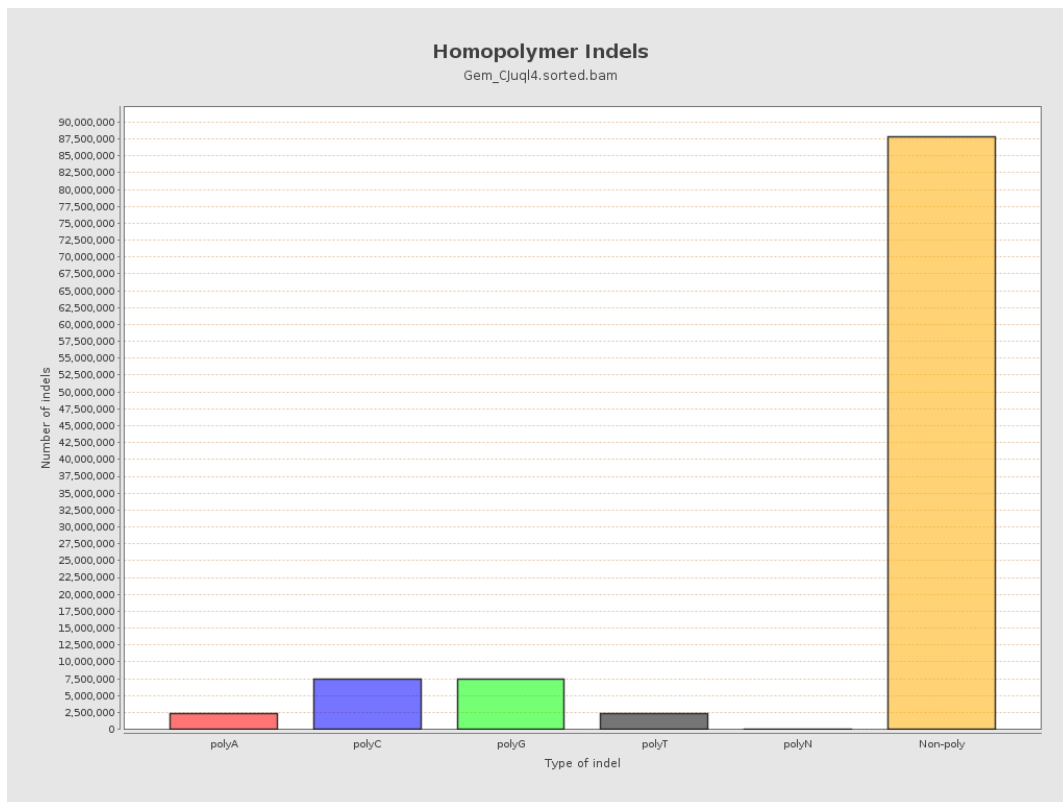
9. Results : Mapped Reads GC-content Distribution



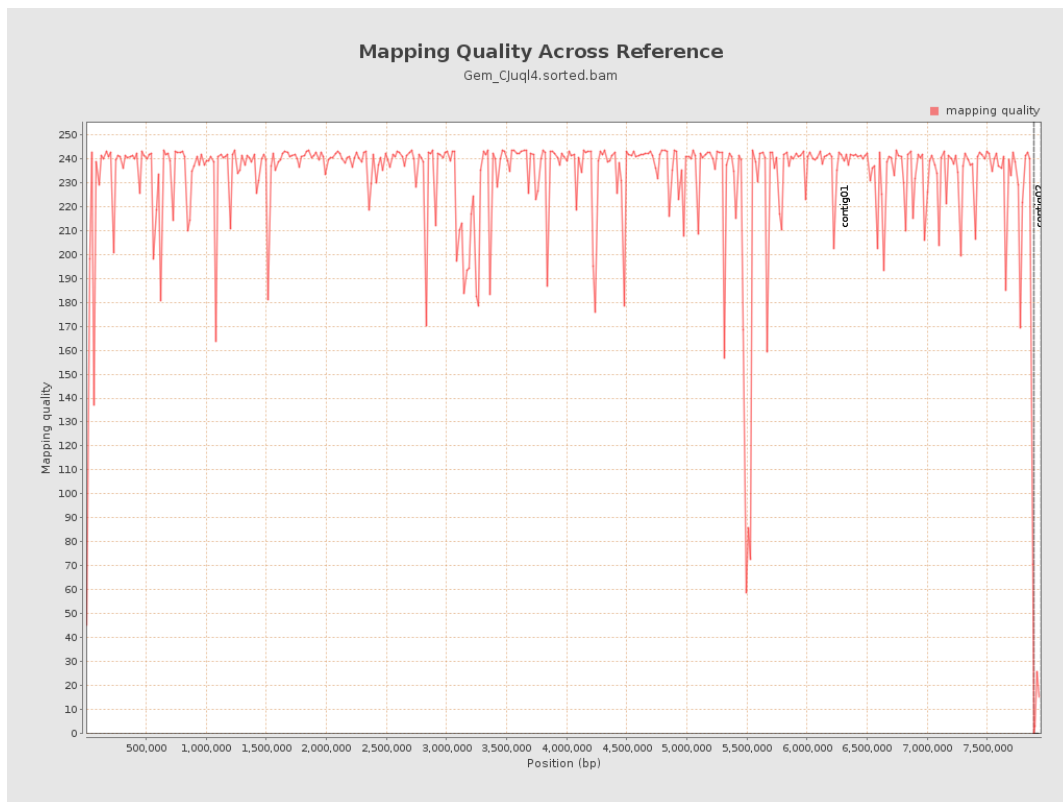
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

